SEQUENCE LISTING

<110> Aventis Pasteur Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-13

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<150> US 60/132,270
<151> 1999-05-03
<150> US 60/141,276
<151> 1999-06-30

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<170> PatentIn Ver. 2.0

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<213> Chlamydia pneumoniae

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Met Val Asn Pro Ile
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr
90 95 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala
105 110 115

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct 499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala
120 125 130

ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct 547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala
135 140 145

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150 155 160 165

gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct 643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala
170 175 180

tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc 691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe
185 190 195

gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa 739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys
200 205 210

gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg 787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly
215 220 225

aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca 835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr
230 235 240 245

gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt 883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe
250 255 260

gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac 931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn
265 270 275

agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag 979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys
280 285 290

aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt 1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu
295 300 305

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310                 315                 320                 325

atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt   1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val
                330                 335                 340

gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc   1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser
            345                 350                 355

atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct   1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser
        360                 365                 370

ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct   1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser
    375                 380                 385

caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc   1315
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390                 395                 400                 405

gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct   1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala
                410                 415                 420

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat   1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn
            425                 430                 435

gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct   1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro
        440                 445                 450

ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag   1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys
    455                 460                 465

acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt   1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly
470                 475                 480                 485

tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat   1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn
                490                 495                 500

gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca   1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr
            505                 510                 515

cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca   1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr
        520                 525                 530
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Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly
    535                 540                 545

gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc   1795
Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile
550                 555                 560                 565

cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca   1843
Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr
                570                 575                 580

tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt   1891
Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu
            585                 590                 595

tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt   1939
Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe
        600                 605                 610

gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa   1987
Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu
    615                 620                 625

acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta   2035
Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu
630                 635                 640                 645

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga          2083
Tyr Ser Gly Tyr Leu Gln
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Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
        35                  40                  45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
    50                  55                  60
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Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
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85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
180 185 190

Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
260 265 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
290 295 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
305 310 315 320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
325 330 335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
340 345 350

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Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
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Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
    370                 375                 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
385                 390                 395                 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
                405                 410                 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
            420                 425                 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
        435                 440                 445

Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val
    450                 455                 460

Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr
465                 470                 475                 480

Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr
                485                 490                 495

Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser
            500                 505                 510

Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg
        515                 520                 525

Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn
    530                 535                 540

Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser
545                 550                 555                 560

Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile
                565                 570                 575

Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr
            580                 585                 590

Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys
        595                 600                 605

Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys
    610                 615                 620

Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val
625                 630                 635                 640
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tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct 96
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro
20 25 30

acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca 144
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr
35 40 45

gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct 192
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala
50 55 60

gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg 240
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala
65 70 75 80

gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat 288
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn
85 90 95

gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat 336
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr
100 105 110

gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc 384
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser
115 120 125

ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac 432
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn
130 135 140

aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca 480
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro
145 150 155 160

ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct 528
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala
165 170 175

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat 576
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr
180 190 195

ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat 624
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn
200 205 210

aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct 672
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala
215 220 225

aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att 720
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile
230 235 240 245

ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa 768
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys
250 255 260

aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca 816
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr
265 270 275

gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt 864
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val
280 285 290

tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg 912
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met
295 300 305

tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat 960
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp
310 315 320 325

tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa 1008
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys
330 335 340

gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa 1056
Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys
345 350 355

gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc 1104
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu
360 365 370

aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt 1152
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val
375 380 385

CCt ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac 1200
Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr
390 395 400 405

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aag acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca 1248
Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala
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ggt tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga 1296
Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg
            425                 430                 435

aat gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc 1344
Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu
        440                 445                 450

aca cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa 1392
Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys
    455                 460                 465

aca gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt 1440
Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu
470                 475                 480                 485

gga gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc 1488
Gly Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile
                490                 495                 500

act cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt 1536
Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu
            505                 510                 515

aca tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa 1584
Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln
        520                 525                 530

ctt tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg 1632
Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu
    535                 540                 545

ttt gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt 1680
Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe
550                 555                 560                 565

gaa acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct 1728
Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser
                570                 575                 580

cta tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga    1779
Leu Tyr Ser Gly Tyr Leu Gln
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35 40 45

Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala
50 55 60

Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala
65 70 75 80

Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn
85 90 95

Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr
100 105 110

Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser
115 120 125

Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn
130 135 140

Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro
145 150 155 160

Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala
165 170 175

Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr
180 185 190

Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn
195 200 205

Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala
210 215 220

Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile
225 230 235 240

Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys
245 250 255

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Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr
            260                 265                 270

Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val
        275                 280                 285

Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met
    290                 295                 300

Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp
305                 310                 315                 320

Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys
                325                 330                 335

Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys
            340                 345                 350

Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu
        355                 360                 365

Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val
    370                 375                 380

Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr
385                 390                 395                 400

Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala
                405                 410                 415

Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg
            420                 425                 430

Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu
        435                 440                 445

Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys
    450                 455                 460

Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu
465                 470                 475                 480

Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile
                485                 490                 495

Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu
            500                 505                 510

Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln
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Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu
    530                 535                 540
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Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe
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                                          Met Val Asn Pro Ile
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ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt  163
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu
                10                  15                  20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct  211
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala
            25                  30                  35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat  259
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp
        40                  45                  50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg  307
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met
    55                  60                  65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct  355
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser
70                  75                  80                  85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg  403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr
                90                  95                  100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct  451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala
            105                 110                 115
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tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct   499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala
        120                 125                 130

ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct   547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala
    135                 140                 145

act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc   595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala
150                 155                 160                 165

gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct   643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala
                170                 175                 180

tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc   691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe
            185                 190                 195

gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa   739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys
        200                 205                 210

gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg   787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly
    215                 220                 225

aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca   835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr
230                 235                 240                 245

gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt   883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe
                250                 255                 260

gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac   931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn
            265                 270                 275

agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag   979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys
        280                 285                 290

aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt   1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu
    295                 300                 305

caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat   1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn
310                 315                 320                 325

atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt   1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val
                330                 335                 340
```

```
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc   1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser
            345                 350                 355

atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct   1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser
        360                 365                 370

ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct   1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser
    375                 380                 385

caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc   1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala
390                 395                 400                 405

gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct   1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala
                410                 415                 420

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat   1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn
            425                 430                 435

gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta       1456
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val
        440                 445                 450
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<210> 6
<211> 452
<212> PRT
<213> Chlamydia pneumoniae

<400> 6

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Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr
  1               5                  10                  15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn
            20                  25                  30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
        35                  40                  45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
    50                  55                  60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
65                  70                  75                  80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
                85                  90                  95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
            100                 105                 110
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Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
180 185 190

Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
260 265 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
290 295 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
305 310 315 320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
325 330 335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
340 345 350

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
355 360 365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
370 375 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
385 390 395 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
435 440 445

Ser Ala Gly Val
450

<210> 7
<211> 2238
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (766)..(2235)

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ttttttgtga aatgtagtgt tgtcgactgg aacacattcg ttccttcaga aacctccact 120

acagaaaaag ctgctacaaa cgctatgaaa tacaaatact gtgtttggca gtggctcgtc 180

ggaaagcata gtcaggttcc ttggatcaat ggacagaaaa agcctctata tctttatgga 240

gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaac 300

ctagcttggt ttattggagg aactttaggg ggactcagaa aagctggaga ctggtctgcc 360

acagtacgtt atgagtatgt cgaagccttg tcggttccag aaatagatgt ttcagggatt 420

ggccgtggta atttattaaa gttttggttc gcccaagcaa ttgctgctaa ctatgatcct 480

aaagaggcta atggttttac aaattataaa ggattttccg ctctatatat gtatggcatc 540

acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaactc 600

ggcagtgatt ttactttccg aaagtttgat ctaggtataa tttcagcgtt ttaagtcaaa 660

ttttaataaa atctttaaaa acaggctcgc attaattatt agtgagagct tttttttat 720

tttttataat aaaactaaaa gatttttatt atttttgag ttttt atg gtt aat cct 777
Met Val Asn Pro
1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp
5 10 15 20

```
ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa   873
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu
                  25                  30                  35

gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc   921
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr
              40                  45                  50

gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc   969
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu
          55                  60                  65

atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct  1017
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser
      70                  75                  80

tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct  1065
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro
  85                  90                  95                 100

acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca  1113
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr
                 105                 110                 115

gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct  1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala
             120                 125                 130

gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg  1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala
         135                 140                 145

gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat  1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn
     150                 155                 160

gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat  1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr
 165                 170                 175                 180

gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc  1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser
                 185                 190                 195

ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac  1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn
             200                 205                 210

aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca  1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro
         215                 220                 225

ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct  1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala
     230                 235                 240
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aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat   1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr
245                 250                 255                 260

ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat   1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn
                265                 270                 275

aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct   1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala
            280                 285                 290

aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att   1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile
        295                 300                 305

ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa   1737
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys
    310                 315                 320

aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca   1785
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr
325                 330                 335                 340

gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt   1833
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val
                345                 350                 355

tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg   1881
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met
            360                 365                 370

tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat   1929
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp
        375                 380                 385

tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa   1977
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys
    390                 395                 400

gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa   2025
Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys
405                 410                 415                 420

gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc   2073
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu
                425                 430                 435

aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta   2121
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val
            440                 445                 450
```

```
ctc ccg ctg cag caa gtt cta tgg atc cga gct cgg tac caa gct tac   2169
Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr
        455                 460                 465

gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac   2217
Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp
    470                 475                 480

cat cat cat cat cat cat tga                                      2238
His His His His His His
485                 490
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<210> 8
<211> 490
<212> PRT
<213> Chlamydia pneumoniae

<400> 8

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Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr
  1               5                  10                  15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn
            20                  25                  30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
        35                  40                  45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
    50                  55                  60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
65                  70                  75                  80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
                85                  90                  95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
            100                 105                 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
        115                 120                 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
    130                 135                 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
145                 150                 155                 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
                165                 170                 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
            180                 185                 190
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Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
260 265 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
290 295 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
305 310 315 320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
325 330 335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
340 345 350

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
355 360 365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
370 375 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
385 390 395 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
435 440 445

Ser Ala Gly Val Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg
450 455 460

Tyr Gln Ala Tyr Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
465 470 475 480

Ser Ala Val Asp His His His His His His
485 490

<210> 9
<211> 43
<212> DNA
<213> primer

<400> 9

ataagaatgc ggccgccacc atggttaatc ctattggtcc agg 43

<210> 10
<211> 35
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<213> primer

<400> 10

gcgccggatc ccttggagat aaccagaata tagag 35

<210> 11
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<212> DNA
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<400> 11

ataagaatgc ggccgccacc atgagtctgg cagataagct ggg 43

<210> 12
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<400> 12

gcgccggatc ccttggagat aaccagaata ta 32

<210> 13
<211> 38
<212> DNA
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<400> 13

gctctagacc gccatgacaa aaaaacatta tgcttggg 38

<210> 14
<211> 28
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<213> primer

<400> 14

cgggatccat agaacttgct gcagcggg 28